Amendments to the Specification:

Please replace the paragraph beginning at page 8, line 3 with the following amended paragraph:

FIG. 2 is a photograph of the results of Northern analysis of maspin expression in human tissue blots. The blots were from Clontech™, Inc. (Palo Alto, CA; Human MTN blot 1 #7760 and Human MTN blot 2 #7759). Each lane contains 2 μg poly A+ RNA from human tissues. 36B4 and actin were used as loading controls.

Please replace the paragraph beginning at page 10, line 34 with the following amended paragraph:

Normal human epithelial cells 70N, 76N, and 81N were from reduction mammoplasties as described by Band et al. (Proc. Natl. Acad. Sci. U.S.A., 86:1249, 1989). Tumor cell lines were obtained from the American Type Culture Collection® (Bethesda, MD). Cell lines in the 21T series were derived from a single patient's tumor cells and are representative of tumor progression. Both normal and tumor cells were cultured in DFCI-1 medium as described by Band et al. (Proc. Natl. Acad. Sci. U.S.A., 86:1249, 1989).

Please replace the paragraph beginning at page 11, line 10 with the following amended paragraph:

Total cellular RNA was prepared as previously described (Swisshelm et al., Cell Growth & Differ., 5:133, 1994). Briefly, 20 μg of total RNA was fractionated on 1% agarose-1.7M formaldehyde gels, transferred to Zetaprobe membrane (BioRad™) in 20x SSC, and baked for 1 hr at 800 C. Blots were probed with a 2.5 kb EcoR1/Xho1 fragment from the maspin cDNA plasmid. 36B4 was used as an internal loading and transfer control.

Please replace the paragraph beginning at page 11, line 20 with the following amended paragraph:

A YAC genomic DNA clone library was screened according to standard techniques with 32P end labeled antisense OL1 as a probe. A positive clone was identified and subcloned into pBluecriptSK™ vector to generate pSKmas1 plasmid. The pSKmas1 was partially sequenced to confirm the presence of promoter, exon 1, and the intron 1 boundary. DNA sequencing was performed using ABI™ 373A Automated DNA sequencer at the core facility of Dana-Farber Cancer Institute.

Please replace the paragraph beginning at page 14, line 1 with the following amended paragraph:

For CAT assays cells were plated at 1.0x106/p100 and grown to about 75% confluence. DNA was transfected by the method of modified DEAE-Dextran (Promega, Madison, WI). The cells were transfected with 10 μg reporter plasmid (except for pCMVCAT where only 2 μg of DNA was used) and 1 μg of pCMVβgal (internal control for transfection efficiency). Forty-eight after transfection cells were harvested in 0.25M Tris(pH 8.5)-15% glycerol and extracts were prepared by three cycles of freeze-thawing. The β-galactosidase activity in the extracts was measured using standard techniques and 20 units of extract were used for each CAT assay (except for the pCMVCAT positive control where only 10 units of extracts were used because of high activity). CAT assay was performed as described by Gorman et al. (Mol. Cel. Biol., 2:1044, 1982). Acetylated chloamphenicol and nonacetylated chloramphenicol was quantitated by cutting out the appropriate regions of the silica gel TLC plate and counting in BioFlour™ (DuPont; Wilmington, DE)

Please replace the paragraph beginning at page 23, line 11 with the following amended paragraph:

We have compared the consensus binding sequence of MAF with that of Ets and found that they share a core binding sequence AGGAAT, which is considered to be the binding site for Ets family transcriptional binding proteins (Werner et al. Cell 83:761, 1995; Wasylyk et al., Nature 346:191, 1990). Therefore, MAF may belong to the Ets family. This possibility is

supported by the EMSA experiment in which MAF binding complexes were competed by several high affinity Ets-binding sites recognized by the majority of the known members of Ets family (Welte et al., Eur. J. Biochem. 223:997, 1994).

Please replace the paragraph beginning at page 24, line 2 with the following amended paragraph:

Total cellular RNA was prepared using standard techniques. 20 μg of total RNA was fractionated on 1% agarose-1.7M formaldehyde gels, transferred to Zetaprobe® (Bio-[[r]]Rad™) membranes in 20xSSC, and baked for 1 hr at 80EC. Blots were probed with a 2.5 kb EcoR1/Xhol fragment from the maspin cDNA plasmid. 364B4 was used as an internal loading and transfer control (Laborda et al., Nucl. Acids. Res. 19:3998, 1991).

Please replace the paragraph beginning at page 25, line 20 with the following amended paragraph:

Cells were plated at 1 x 106/p100 and grown to about 75% confluence. SNA was transfected by the method of modified DEAE-Dextran (Promega, Inc., Madison, WI). The amounts of DNAs used were: 10 μg reporter plasmid, except for pCMVCAT in which only 2 μg of DNA was used. 1 μg of pCMVβgal was used as an internal control for transfection efficiency. For the androgen treatment, 50 nM methyltrienolone (R1881, from Du Pont-New England Nuclear, Inc., Boston, MA) or vehicle was added to the cultures after transfection. Forty eight hrs after transfection, cells were harvested in 0.25M Tris(pH 8.5)-15% glycerol. The extracts were made by three cycles of freeze-thaw. The β-galactosidase activity in the extracts was calculated as described by Swisshelm et al. (Cell Growth Differ. 5:133, 1994). Twenty units of extracts (calculated by β-galactosidase activity) were used for each CAT assay except for transfection with pCMVCAT positive control in which only 10 units of extracts were used because of high activity. CAT assay was performed as described by Gorman et al. (Mol. Cell. Biol. 2:1044, 1982). Quantitation of acetylated CoA and nonacetylated chloramphenicol was performed by cutting out the appropriate regions of the silica gel TLC plate and counting in BioFluor (DuPont, Wilmington, DE).

Please replace the paragraph beginning at page 26, line 10 with the following amended paragraph:

Nuclear extracts were made as described by Dignam et al. Nucl. Acids Res. 11:1475, 1983. Binding reactions were carried out at room temperature for 30 minutes in a mixture containing 4% glycerol, 1mM MgCl2, 0.2 mM EDTA, 0.5 mM DTT, 50 mM NaCl, 10 mM Tris-Cl, 2 μg poly (dI-dC), 50 nM R1881, 10 μg nuclear extracts, and end-labeled oligonucleotide probe. Monoclonal (rat) anti-androgen receptor antibody (MAI-150) was purchased from Affinity Bioreagents, Inc. Antibody against glucocorticoid receptor was purchased from Santa Cruz Biotechnology, Inc. Rat IgG negative control was purchased from Sigma. The complexes were subjected to electrophoresis at 5% acrylamide gel in 0.5x Tris-Borate-EDTA buffer.